



I HEREBY CERTIFY THAT THIS CORRESPONDENCE IS BEING DEPOSITED WITH THE UNITED STATES POSTAL SERVICE FIRST CLASS MAIL IN AN ENVELOPE ADDRESSED TO: COMMISSIONER FOR PATENTS, P.O. BOX 1450, ALEXANDRIA, VA 22313-1450, ON THE DATE INDICATED BELOW.

BY: Helene Ito Date: March 9, 2006

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

First Named Inventor:	Nobuya ITOH	§	Group Art Unit: 1652
		§	
		§	
Conf. No.:	7835	§	Examiner: Kagnew H. Gebreyesus, Ph.D.
		§	
Appln. No.:	10/782,998	§	Allowed December 22, 2005
		§	
Filing Date:	February 20, 2004	§	Attorney Docket No.: 600630-15US
		§	(562737)
Title:	REDUCTASE GENE AND USE OF THE SAME		

**DECLARATION OF NOBUYA ITOH**  
**REGARDING REPLACEMENT SEQUENCE LISTINGS**

I, Nobuya Itoh, hereby declare as follows:

1. I am the inventor and applicant in the above-identified patent application.

2. Upon reviewing the Notice of Allowance dated December 22, 2005, concerning this application. I realized that corrections to the Sequence Listings for SEQ ID NOS:1 and 2 which had been identified earlier had never been made during the prosecution of this application. I realized that there were errors when I started another study about the gene of the present invention and analyzed the nucleotide sequences in the same way repeatedly, thereby noticing some mistakes in the sequences.

3. The errors occurred as a result of simple mistakes when analyzing the nucleotide sequence of SEQ ID NO:2 with an ABI Prism 310 Genetic Analyzer, where the mistakes are identified as follows:

1. 123<sup>rd</sup> Nucleotide: Peak of "C" was buried by peak "A" due to succession of "A".
2. 246<sup>th</sup> Nucleotide: Peak of "A" was confirmed by performing analysis again.

3. 467<sup>th</sup> Nucleotide: Peak of "C" was buried by peak "G" due to continuation of "G" and "C".
4. 593<sup>rd</sup> Nucleotide: Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".
5. 595<sup>th</sup> Nucleotide: Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".
6. 617<sup>th</sup> Nucleotide: Peak of "C" was buried by peak "T" due to continuation of "T" and "C".
7. 620<sup>th</sup> Nucleotide: Peak of "G" was buried due to succession of "A" and "G" and low sensitivity of peak "G".
8. 692<sup>nd</sup> Nucleotide: Peak of "G" was confirmed by performing analysis again.

4. Attached is a copy of a ClustalW Formatted Alignments printout showing the eight mistakes identified in paragraph 3 above. Also attached is a comparison of the original and amended nucleotide sequence for SEQ ID NO:2.

5. The errors were inadvertent and without any disceptive intention.

6. Since the DNA of SEQ ID NO:2 is from the same *Leifsonia* sp. S-749 (Accession No. of International Depositary Authority: FERM BP-8291) as set forth in the application, no new matter has been added by correcting the nucleotide sequence of the DNA in SEQ ID NO:2.

7. In view of the corrections made to SEQ ID NO:2, the corresponding amino acids of SEQ ID NO:1 coded by the DNA of SEQ ID NO:2 also required correction. The corrections are noted in the attached comparison of the original amino acid sequence and the amended amino acid sequence for SEQ ID NO:1. For the same reasons as mentioned in paragraph 6, although corrections have been made to the amino acid sequence, no new matter has been added.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States

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Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

NOBUYA ITOH

March 9, 2006  
(Date)

Nobuya Itoh

20040606old PTKR Aligned Seq... Formatted Alignment  
200428 Tue 231 1 011 5:12 PM

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ClustalW Formatted Alignments

20040606old PTKR	A T G G C T C A G T A C G A C G T C G C C G A C C G A T C C G C G A T C G T G A C C G G A G G C C G	10	20	30	40	50
20040617newPTKR	A T G G C T C A G T A C G A C G T C G C C G A C C G A T C C G C G A T C G T G A C C G G A G G C C G	10	20	30	40	50
20040606old PTKR	C T C G G C A T C G G G C G C C C G T G C G C T C A C T C T C G C G G C G A G C G G C G A G	60	70	80	90	100
20040617newPTKR	C T C G G C A T C G G G C G C C C G T G C G C T C A C T C T C G C G G C G A G C G G C G A G	60	70	80	90	100
20040606old PTKR	C C T C C T C G T C A C C G A C C T G A A G A G G A G C A C G C G C A G G C C G T C G T G G C C	110	120	130	140	150
20040617newPTKR	C C T C C T C G T C A C C G A C C T G A A G A G G A G C A C G C G C A G G C C G T C G T G G C C	110	120	130	140	150
20040606old PTKR	G A G A T C G A G G C C C G C G G C G G T A A G G C C G C C G C G C T C G C G G G C A C G T G A C	160	170	180	190	200
20040617newPTKR	G A G A T C G A G G C C C G C G G C G G T A A G G C C G C C G C G C T C G C G G G C A C G T G A C	160	170	180	190	200
20040606old PTKR	C C T C A A G A T C G C G G T C A A C A A C G C G G G C A T C G G C G G C G A G G C C G C C A C G	210	220	230	240	250
20040617newPTKR	C C T C A A G A T C G C G G T C A A C A A C G C G G G C A T C G G C G G C G A G G C C G C C A C G	210	220	230	240	250
20040606old PTKR	C C T C A A G A T C G C G G T C A A C A A C G C G G G C A T C G G C G G C G A G G C C G C C A C G	260	270	280	290	300
20040617newPTKR	C C T C A A G A T C G C G G T C A A C A A C G C G G G C A T C G G C G G C G A G G C C G C C A C G	260	270	280	290	300
20040606old PTKR	G T C G G C G A C T A C T C G C T C G A C A G C T G G C G C A C G G T G A T C G A G G T C A A C C T	310	320	330	340	350
20040617newPTKR	G T C G G C G A C T A C T C G C T C G A C A G C T G G C G C A C G G T G A T C G A G G T C A A C C T	310	320	330	340	350
20040606old PTKR	C A A C G C C G T G T T C T A C G G G A T G C A G C C G C A G C T G A A G G C C A T G G C C G C C A	360	370	380	390	400
20040617newPTKR	C A A C G C C G T G T T C T A C G G G A T G C A G C C G C A G C T G A A G G C C A T G G C C G C C A	360	370	380	390	400
20040606old PTKR	A C G G C G G C G G T G C G A T C G T C A A C A T G G C G T C C A T C C T G G G A A G C G T C G G C	410	420	430	440	450
20040617newPTKR	A C G G C G G C G G T G C G A T C G T C A A C A T G G C G T C C A T C C T G G G A A G C G T C G G C	410	420	430	440	450
20040606old PTKR	T T C G C C A A C T C G T C G C T A C G T C A C G G C C A A G C A C G C G C T G C T C G G T C T	460	470	480	490	500
20040617newPTKR	T T C G C C A A C T C G T C G C T A C G T C A C G G C C A A G C A C G C G C T G C T C G G T C T	460	470	480	490	500
20040606old PTKR	C A C C C A G A A C G C C G C C T C G A G T A C G C C G C C G A C A A G G T G G C G C T C G T C G	510	520	530	540	550
20040617newPTKR	C A C C C A G A A C G C C G C C T C G A G T A C G C C G C C G A C A A G G T G G C G C T C G T C G	510	520	530	540	550
20040606old PTKR	C G G T C G G C C C G G C T C A T C C G C A C C C G C T C G T G G A G G C A A T T T C G G C	560	570	580	590	600
20040617newPTKR	C G G T C G G C C C G G C T C A T C C G C A C C C G C T C G T G G A G G C A A T T T C G G C	560	570	580	590	600
20040606old PTKR	C G A C G C G C T G G C G T C T A A G G A A G A A G C C C T C G G C C G C C T G G G C G A	610	620	630	640	650
20040617newPTKR	C G A C G C G C T G G C G T C T A A G G A A G A A G C C C T C G G C C G C C T G G G C G A	610	620	630	640	650
20040606old PTKR	E C C G G A A G A G G T C G C C T C G C T G G T C G C G T T C C T C G C C T E C G C C G C G A	660	670	680	690	700
20040617newPTKR	E C C G G A A G A G G T C G C C T C G C T G G T C G C G T T C C T C G C C T E C G C C G C G A	660	670	680	690	700
20040606old PTKR	G C T T C A T C A C C G G C A G C T A C C A C C T G G T G G A C G G C G G C T A C A C C G C C A G	710	720	730	740	750
20040617newPTKR	G C T T C A T C A C C G G C A G C T A C C A C C T G G T G G A C G G C G G C T A C A C C G C C A G	710	720	730	740	750
20040606old PTKR	T G A	760	770	780	790	800
20040617newPTKR	T G A	760	770	780	790	800

(A)

(B)

(C)

Original nucleotide sequence

## Amended nucleotide sequence

70 80 90 100 110 120  
gggcgcgccgtggcgctcaactctcgcgagcgcgcgcgcgtcctcgtcacccacctg

gcgctcgggcgacgtgacccgacccgcgttcggcgaggcgagcgtcgccggggcgac

gtcggcgactactcgctcgacagctggcgacggtgatcgagggtcaacctcaacgcgctg

430 440 450 460 470 480  
aacatggcgtccatcctctgggaagcgtcggcttcgccactcgtgggcacgtcagcc

550 560 570 580 590 600  
cgcgtcgcgggtcgcccggttcaccgcaccgcctcgtgaggcaacttctcgg

gtgcctgcctggctgcggttctctgccttcgacccgcgcgagcttcaccgcgcagctad

	730	740	750
	cacctggtggacggcggtacacggccagtga		

70 80 90 100 110 120  
gggcgcgcgtggcgcctcaactctcgcgcgcagcgcgcacgcctcctctcaccgaactg

gcgctcgcgggcgacgtgaccgaccccggttcggcgaggcgagcgtcgccggggcggaac

gtcggcgactactcgcctcgacagctggcgacggtgatcgagggtcaacctcaacgcgctg

430 440 450 460 470 480  
aacatggcgtccatcctcgggaagcgtcggttcgccaaactcgtcgcctacgtcagggcc

550 560 570 580 590 600  
cgcgctgcgcggtcggcccccgggttcattccgacccgctcgtggaggcaacctctccgc

670 680 690 700 710 720  
tcgcctcgctggtcgcggttcctcgcctcgcgcgcgcgagcttcattcacccggcagctac

acctggtggacggcggtacacggccagtga

SEQ ID NO: 1

## Original amino acid sequence

10 MetAlaGlnTyrAspValAlaAspArgSerAlaIleValThrGlyGlySerGlyIle 20  
30 GlyArgAlaValAlaLeuThrLeuAlaAlaSerGlyAlaAlaValLeuValThrAspLeu 40  
50 **Lys**GluGluHisAlaGlnAlaValValAlaGluIleGluAlaAlaGlyGlyLysAlaAla 60  
70 AlaLeuAlaGlyAspValThrAspProAlaPheGlyGluAlaSerValAlaGlyAlaAsn 80  
90 AlaLeuAlaProLeuLysIleAlaValAsnAlaGlyIleGlyGlyGluAlaAlaThr 100  
110 ValGlyAspTyrSerLeuAspSerTrpArgThrValIleGluValAsnLeuAsnAlaVal 120  
130 PheTyrGlyMetGlnProGlnLeuLysAlaMetAlaAlaAsnGlyGlyAlaIleVal 140  
150 AsnMetAlaSerIleLeuGlySerValGlyPheAlaAsnSer**Gly**TyrValThrAla 160  
170 LysHisAlaLeuGlyLeuThrGlnAsnAlaAlaLeuGluTyrAlaAlaAspLysVal 180  
190 ArgValValAlaValGlyProGlyPheIleArgThrArgSerTrpArgGln**Leu**PheArg 200  
210 ArgArgAlaGlyVal**Leu**GlnGlyLysHisAlaLeuGlyArgLeuGlyGluProGluGlu 220  
230 ValAlaSerLeuValAlaPheLeuAlaSer**Asp**AlaAlaSerPheIleThrGlySerTyr 240  
250 HisLeuValAspGlyGlyTyrThrAlaGln

41 **Lys** ⇒ **Asn**

156 **Gly** ⇒ **Ala**

198 **Leu** ⇒ **Pro**

199 **Phe** ⇒ **Leu**

206 **Leu** ⇒ **Pro**

207 **Gln** ⇒ **Arg**

231 **Asp** ⇒ **Gly**

## Amended amino acid sequence

10 MetAlaGlnTyrAspValAlaAspArgSerAlaIleValThrGlyGlySerGlyIle 20  
30 GlyArgAlaValAlaLeuThrLeuAlaAlaSerGlyAlaAlaValLeuValThrAspLeu 40  
50 **Asn**GluGluHisAlaGlnAlaValValAlaGluIleGluAlaAlaGlyGlyLysAlaAla 60  
70 AlaLeuAlaGlyAspValThrAspProAlaPheGlyGluAlaSerValAlaGlyAlaAsn 80  
90 AlaLeuAlaProLeuLysIleAlaValAsnAlaGlyIleGlyGlyGluAlaAlaThr 100  
110 ValGlyAspTyrSerLeuAspSerTrpArgThrValIleGluValAsnLeuAsnAlaVal 120  
130 PheTyrGlyMetGlnProGlnLeuLysAlaMetAlaAlaAsnGlyGlyAlaIleVal 140  
150 AsnMetAlaSerIleLeuGlySerValGlyPheAlaAsnSer**Ala**TyrValThrAla 160  
170 LysHisAlaLeuGlyLeuThrGlnAsnAlaAlaLeuGluTyrAlaAlaAspLysVal 180  
190 ArgValValAlaValGlyProGlyPheIleArgThrArgSerTrpArgGln**Pro**LeuArg 200  
210 ArgArgAlaGlyVal**Pro**ArgGlyLysHisAlaLeuGlyArgLeuGlyGluProGluGlu 220  
230 ValAlaSerLeuValAlaPheLeuAlaSer**Gly**AlaAlaSerPheIleThrGlySerTyr 240  
250 HisLeuValAspGlyGlyTyrThrAlaGln